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OFFICE OF PETITIONS



1600

RAW SEQUENCE LISTING

DATE: 04/21/2004

PATENT APPLICATION: US/09/933,915A

TIME: 07:09:44

Input Set : A:\07917-120001.txt

Output Set: N:\CRF4\04212004\I933915A.raw

4 <110> APPLICANT: Odgren, Paul R.
5 Marks, Sandy C.
6 Choi, Yongwon
8 <120> TITLE OF INVENTION: TRANCE REGULATION OF CHONDROCYTE
9 DIFFERENTIATION
11 <130> FILE REFERENCE: 07917-120001
13 <140> CURRENT APPLICATION NUMBER: 09/933,915A
14 <141> CURRENT FILING DATE: 2001-08-20
16 <150> PRIOR APPLICATION NUMBER: 60/226,197
17 <151> PRIOR FILING DATE: 2000-08-18
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2226
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (157)...(1107)
32 <400> SEQUENCE: 1

33 ctcgacccac gcgctccgcgc gccccaggag ccaaagccgg gctccaagtc ggcgccccac 60
34 gtcgaggctc cgccgcagcc tccggagttg gccgcagaca agaaggggag ggagcgggag 120
35 agggaggaga gctccgaagc gagagggccg agcgcc atg cgc cgc gcc agc aga 174
36 Met Arg Arg Ala Ser Arg
37 1 5
39 gac tac acc aag tac ctg cgt ggc tcg gag gag atg ggc ggc ggc ccc 222
40 Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu Glu Met Gly Gly Gly Pro
41 10 15 20
43 gga gcc ccg cac gag ggc ccc ctg cac gcc ccg ccg ccg cct gcg ccg 270
44 Gly Ala Pro His Glu Gly Pro Leu His Ala Pro Pro Pro Pro Ala Pro
45 25 30 35
47 cac cag ccc ccc gcc gcc tcc cgc tcc atg ttc gtg gcc ctc ctg ggg 318
48 His Gln Pro Pro Ala Ala Ser Arg Ser Met Phe Val Ala Leu Leu Gly
49 40 45 50
51 ctg ggg ctg ggc cag gtt gtc tgc agc gtc gcc ctg ttc ttc tat ttc 366
52 Leu Gly Leu Gly Gln Val Val Cys Ser Val Ala Leu Phe Phe Tyr Phe
53 55 60 65 70
55 aga gcg cag atg gat cct aat aga ata tca gaa gat ggc act cac tgc 414
56 Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys
57 75 80 85
59 att tat aga att ttg aga ctc cat gaa aat gca gat ttt caa gac aca 462
60 Ile Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr
61 90 95 100

P.6
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63	act	ctg	gag	agt	caa	gat	aca	aaa	tta	ata	cct	gat	tca	tgt	agg	aga	510
64	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile	Pro	Asp	Ser	Cys	Arg	Arg	
65			105					110					115				
67	att	aaa	cag	gcc	ttt	caa	gga	gct	gtg	caa	aag	gaa	tta	caa	cat	atc	558
68	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	
69		120					125					130					
71	gtt	gga	tca	cag	cac	atc	aga	gca	gag	aaa	gcg	atg	gtg	gat	ggc	tca	606
72	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys	Ala	Met	Val	Asp	Gly	Ser	
73	135					140					145				150		
75	tgg	tta	gat	ctg	gcc	aag	agg	agc	aag	ctt	gaa	gct	cag	cct	ttt	gct	654
76	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	
77					155					160				165			
79	cat	ctc	act	att	aat	gcc	acc	gac	atc	cca	tct	ggg	tcc	cat	aaa	gtg	702
80	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	
81			170						175				180				
83	agt	ctg	tcc	tct	tgg	tac	cat	gat	cgg	ggg	tgg	gcc	aag	atc	tcc	aac	750
84	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	
85		185						190					195				
87	atg	act	ttt	agc	aat	gga	aaa	cta	ata	gtt	aat	cag	gat	ggc	ttt	tat	798
88	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val	Asn	Gln	Asp	Gly	Phe	Tyr	
89		200				205					210						
91	tac	ctg	tat	gcc	aac	att	tgc	ttt	cga	cat	cat	gaa	act	tca	gga	gac	846
92	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Asp	
93	215				220					225				230			
95	cta	gct	aca	gag	tat	ctt	caa	cta	atg	gtg	tac	gtc	act	aaa	acc	agc	894
96	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Thr	Lys	Thr	Ser	
97			235					240					245				
99	atc	aaa	atc	cca	agt	tct	cat	acc	ctg	atg	aaa	gga	gga	agc	acc	aag	942
100	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	
101			250					255				260					
103	tat	tgg	tca	ggg	aat	tct	gaa	ttc	cat	ttt	tat	tcc	ata	aac	gtt	ggg	990
104	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	
105		265					270					275					
107	gga	ttt	ttt	aag	tta	cgg	tct	gga	gag	gaa	atc	agc	atc	gag	gtc	tcc	1038
108	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu	Ile	Ser	Ile	Glu	Val	Ser	
109		280				285					290						
111	aac	ccc	tcc	tta	ctg	gat	cgg	gat	cag	gat	gca	aca	tac	ttt	ggg	gct	1086
112	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	
113	295				300				305				310				
115	ttt	aaa	gtt	cga	gat	ata	gat	tgagccccag	tttttggagt	gttatgtatt							1137
116	Phe	Lys	Val	Arg	Asp	Ile	Asp										
117			315														
119	tcctggatgt	ttggaacat	tttttaaaac	aagccaagaa	agatgtatat	aggtgtgtga											1197
120	gactactaag	aggcatggcc	ccaacgggtac	acgactcagt	atccatgctc	ttgaccttgt											1257
121	agagaacacg	cgtattttaca	gccagtggga	gatgttagac	tcatgggtgtg	ttacacaatg											1317
122	gttttttaaat	tttgtaatga	attcctagaa	ttaaaccaga	ttggagcaat	tacgggttga											1377
123	ccttatgaga	aactgcatgt	gggctatggg	aggggttggg	ccctgggcat	gtgcccccttc											1437
124	gcagctgaag	tggagagggt	gtcatctagc	gcaattgaag	gatcatctga	agggggcaaat											1497
125	tcttttgaat	tgttacatca	tgctggaacc	tgcaaaaaat	acttttttcta	atgaggagag											1557

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```

126 aaaatatatg tttttttata taatatctaa agttatatatt cagatgtaat gttttctttg 1617
127 caaagtattg taaattatat ttgtgctata gtatttgatt caaaatattt aaaaatgtct 1677
128 tgctgttgac atatttaatg ttttaaagt acagacatat ttaactgggt cactttgtaa 1737
129 attccctggg gaaaacttgc agctaaggag gggaaaaaaa tgttgtttcc taatatcaaa 1797
130 tgcagtatat ttcttcgttc tttttaagtt aatagatttt ttcagacttg tcaagcctgt 1857
131 gcaaaaaaat taaaatggat gccttgaata ataagcagga tgttggccac caggtgcctt 1917
132 tcaaatttag aaactaattg actttagaaa gctgacattg ccaaaaagga tacataatgg 1977
133 gccactgaaa tctgtcaaga gtagttatat aattgttgaa caggtgtttt tccacaagtg 2037
134 ccgcaaattg tacctttttt tttttttcaa aatagaaaag ttattagtgg tttatcagca 2097
135 aaaaagtcca attttaattt agtaaagtgt atcttatact gtacaataaa aacattgcct 2157
136 ttgaatgtta attttttggg acaaaaaataa atttatatga aaacctgaaa aaaaaaacaa 2217
137 aaaaaaaaaa 2226
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 317
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
145 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
146 1 5 10 15
147 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
148 20 25 30
149 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
150 35 40 45
151 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
152 50 55 60
153 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
154 65 70 75 80
155 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
156 85 90 95
157 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
158 100 105 110
159 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
160 115 120 125
161 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
162 130 135 140
163 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
164 145 150 155 160
165 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
166 165 170 175
167 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
168 180 185 190
169 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
170 195 200 205
171 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
172 210 215 220
173 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
174 225 230 235 240
175 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
176 245 250 255

```

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177 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 178 260 265 270
 179 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 180 275 280 285
 181 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 182 290 295 300
 183 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 184 305 310 315

186 <210> SEQ ID NO: 3

187 <211> LENGTH: 192

188 <212> TYPE: PRT

189 <213> ORGANISM: Homo Sapiens

191 <400> SEQUENCE: 3

192 Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg
 193 1 5 10 15
 194 Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg
 195 20 25 30
 196 Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr
 197 35 40 45
 198 Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His
 199 50 55 60
 200 Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys
 201 65 70 75 80
 202 Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys
 203 85 90 95
 204 Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln
 205 100 105 110
 206 Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His
 207 115 120 125
 208 Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu
 209 130 135 140
 210 Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser
 211 145 150 155 160
 212 Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro
 213 165 170 175
 214 Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 215 180 185 190

217 <210> SEQ ID NO: 4

218 <211> LENGTH: 181

219 <212> TYPE: PRT

220 <213> ORGANISM: Homo sapiens

222 <400> SEQUENCE: 4

223 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
 224 1 5 10 15
 225 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
 226 20 25 30
 227 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
 228 35 40 45
 229 Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr

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```

230      50      55      60
231 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
232 65      70      75      80
233 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
234      85      90      95
235 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
236      100      105      110
237 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
238      115      120      125
239 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
240      130      135      140
241 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
242 145      150      155      160
243 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
244      165      170      175
245 Val Arg Asp Ile Asp
246      180
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 178
250 <212> TYPE: PRT
251 <213> ORGANISM: Homo sapiens
253 <400> SEQUENCE: 5
254 Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala
255 1      5      10      15
256 Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
257      20      25      30
258 Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp
259      35      40      45
260 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn
261      50      55      60
262 Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
263 65      70      75      80
264 Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr
265      85      90      95
266 Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser
267      100      105      110
268 Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn
269      115      120      125
270 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
271      130      135      140
272 Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu
273 145      150      155      160
274 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp
275      165      170      175
276 Ile Asp
279 <210> SEQ ID NO: 6
280 <211> LENGTH: 173
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/933,915A

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Base Note:

Presence of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 4,9,12

VERIFICATION SUMMARY

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375 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9

376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0